

IN THE SPECIFICATION

Please amend paragraph [0046] of the specification, beginning on page 25, as follows:

[0046] The methods described above can be used to identify binding modes of a set of ligands for which affinity has been measured experimentally. The binding modes can be characterized using the amino acids that make direct electrostatic or ~~vander-Waal's~~ van der Waals contact with, or form hydrogen bonds with, the ligand and the importance of these residues in binding can be tested experimentally by point mutation studies. Once the critical amino acids that contribute to the binding of the ligand are identified, the distances between those amino acids and the bound ligand and between the amino acids themselves can be measured to generate a distance map. This distance map can be used according to known techniques to derive a pharmacophore model — a geometric model representing a pattern of features that are (or are predicted to be) required for binding with the protein.